SEQUENCE LISTING

<110>   Buck, Linda B
         Axel, Richard

<120>   Odorant Receptors and Uses Thereof

<130>   38586-B

<140>   US 09/771,209
<141>   2001-01-26

<150>   US 08/129,079
<151>   1993-10-05

<160>   98

<170>   PatentIn version 3.1

<210>   1
<211>   954
<212>   DNA
<213>   Rattus sp.

<400>   1
atggaatcag ggaacagcac aagaagattt tcaagttttt ttcttcttgg atttacagaa   60

aacccacaac ttcacttcct catttttgca ctattcctgt ccatgtacct ggtaacagtg   120

cttgggaacc tgcttatcat tatggccatc atcacacagt ctcatttgca tacacccatg   180

tactttttcc ttgctaacct atcctttgtg gacatctgtt tcacctccac caccatccca   240

aagatgttgg taaatatata cacccagagc aagagcatca cctatgaaga ctgtattagc   300

cagatgtgtg tcttcttggt tttcgcagaa ttgggcaact ttctcctggc tgtgatggcc   360

tatgaccgat atgtggctaa ctgtcaccca ctgtgttaca cagtcattgt gaaccaccgg   420

ctctgtatcc tgctgcttct gctgtcctgg gttatcagca ttttccatgc cttcatacag   480

agcttaattg tgctacagtt gaccttctgt ggagatgtga aaatccctca cttcttctgt   540

gaacttaatc agctgtccca actcacctgt tcagacaact ttccaagtca cctcataatg   600

aatcttgtac ctgttatgtt ggcagccatt ccttcagtg catccttta ctcttatttc   660

aagatagtat cctccataca ttctatctcc acagttcagg ggaagtacaa ggcattttct   720

acttgtgcct ctcacctttc cattgtctcc ttattttata gtacaggcct cggagtgtac   780

gtcagttctg ctgtggtcca aagctcacat tctgctgcaa gtgcttcggt catgtatact   840

gtggtcaccc ccatgctgaa ccccttcatt tatagtctaa ggaataaaga tgtgaagaga   900

gctctggaaa gactgttaga aggaaactgt aaagtgcatc attggactgg atga   954

<210> 2
<211> 1002
<212> DNA
<213> Rattus sp.

<400> 2
atggactcaa gcaacaggac aagagtttca gaatttcttc ttcttggatt tgtagaaaac   60

aaagacctac aaccccttat ttatggtctt tttctctcta tgtacctggt tactgtcatt   120

ggaaacatat ccattattgt ggctatcatt tcagatccct gtctgcacac ccccatgtat   180

ttcttcctct ctaacctgtc ctttgtggac atctgtttca tttcaaccac tgttccaaag   240

atgttagtga acatccagac ccaaaacaat gtcatcacct atgcaggatg cattacccag   300

atatactttt tcttgctctt tgtagaattg gacaacttct tgctgactat catggcctat   360

gaccgttacg tagccatctg tcaccccatg cactacacag ttatcatgaa ctacaagctc   420

tgtggatttc tggttctggt atcttggatt gtaagtgttc tgcatgcctt gtttcaaagc   480

ttgatgatgt tggcgctgcc cttctgcaca catctggaaa tcccacacta cttctgtgaa   540

cctaatcagg tgattcaact cacctgttct gatgcatttc ttaatgatct tgtgatatat   600

tttacacttg tgctgctggc tactgttcct cttgctggca tcttctattc ttacttcaag   660

atagtgtcct ccatatgtgc tatatcgtca gttcatggga agtacaaagc attctccacc   720

tgtgcatctc acctttcagt cgtgtcttta ttttactgca caggactagg agtgtacctc   780

agttctgctg caaacaacag ctcacaggca agtgccacag cctcagtcat gtacactgta   840

gttacccctaa tggtgaaccc ttttatctat agtcttagga ataaagatgt taagagtgtt   900

ctgaaaaaaa ctctttgtga ggaagttata aggagtccac cttccctact tcatttcttc   960

ctagtgttat gtcatctccc ttgtttattt ttttgttatt aa   1002

<210> 3
<211> 942
<212> DNA
<213> Rattus sp.

<400> 3
atgagcagca ccaaccagtc cagtgtcacc gagttcctcc tcctgggact ctccaggcag   60

ccccagcagc agcagctcct cttcctgctc ttcctcatca tgtacctggc cactgtcctg   120

ggaaacctgc tcatcatcct ggctattggc acagactccc gcctgcacac ccccatgtac   180

ttcttcctca gtaacctgtc ctttgtggat gtctgcttct cctctaccac tgtccctaaa   240

gttctggcca accatatact tgggagtcag gccatttcct tctctgggtg tctcacccag   300

```
ctgtattttc tcgctgtgtt tggtaacatg gacaatttcc tgctggctgt gatgtcctat      360

gaccgatttg tggccatatg ccaccctttta cactacacaa caaagatgac ccgtcagctc      420

tgtgtcctgc ttgttgtggg gtcatgggtt gtagccaaca tgaattgtct gttgcacata      480

ctgctcatgg ctcgactctc cttctgtgca gacaacatga tcccccactt cttctgtgat      540

ggaactcccc tcctgaaact ctcctgctca gacacacatc tcaatgagct gatgattctt      600

acagagggag ctgtggtcat ggtcacccca tttgtctgca tcctcatctc ctacatccac      660

atcacctgtg ctgtcctcag agtctcatcc cccaggggag gatggaaatc cttctccacc      720

tgtggctccc acctggctgt ggtctgcctc ttctatggca ccgtcatcgc tgtgtatttc      780

aacccatcat cctctcactt agctgggagg gacatggcag ctgcagtgat gtatgcagtg      840

gtgaccccaa tgctgaaccc tttcatctat agcctgagga acagcgacat gaaagcagct      900

ttaaggaaag tgctcgccat gagatttcca tctaagcagt aa                         942
```

<210> 4
<211> 936
<212> DNA
<213> Rattus sp.

<400> 4
```
atggcttgga gtactggcca gaacctgtcc acaccaggac cattcatctt gctgggcttc       60

ccagggccaa ggagcatgcg cattgggctc ttcctgcttt tcctggtcat gtatctgctt      120

acggtagttg gaaacctagc catcatctcc ctggtaggtg cccacagatg cctacagaca      180

cccatgtact tcttcctctg caacctctcc ttcctggaga tctggttcac cacagcctgc      240

gtacccaaga ccctggccac atttgcgcct cggggtggag tcatttcctt ggctggctgt      300

gccacacaga tgtactttgt cttttctttg ggctgtaccg agtacttcct gctggctgtg      360

atggcttatg accgctacct ggccatctgc ctgccactgc gctatggtgg catcatgact      420

cctgggctgg cgatgcggtt ggccctggga tcctggctgt gtgggttttc tgcaatcaca      480

gttcctgcta ccctcattgc ccgcctctct ttctgtggct cacgtgtcat caaccacttc      540

ttctgtgaca tttcgccctg gatagtgctt tcctgcaccg acacgcaggt ggtggaactg      600

gtgtcctttg gcattgcctt ctgtgttatt ctgggctcgt gtggtatcac actagtctcc      660

tatgcttaca tcatcactac catcatcaag attccctctg cccggggccg gcaccgcgcc      720

ttctcaacct gctcatccca tctcactgtg gtgctgattt ggtatggctc caccatcttc      780

ttgcatgtga ggacctcggt agagagctcc ttggacctca ccaaagctat cacagtgctc      840
```

```
aacaccattg tcacacctgt gctgaaccct ttcatatata ctctgaggaa caaggatgtc      900

aaggaagctc tgcgcaggac ggtgaagggg aagtga                                936


<210>   5
<211>   939
<212>   DNA
<213>   Rattus sp.

<400>   5
atgactggaa ataaccaaac tttgatcttg gagttcctcc tcctgggtct gcccatccca      60

tcagagtatc atctcctgtt ctatgccctg ttcctggcca tgtacctcac catcatcctg      120

ggaaacctgc taatcattgt ccttgttcga ctggactctc atctccacat gcccatgtac      180

ttgtttctca gcaacttgtc cttctctgac ctctgctttt cctctgtcac aatgcccaaa      240

ttgcttcaga acatgcagag ccaagtacca tctatatcct atacaggctg cctgacacag      300

ctgtacttct ttatggtttt tggagatatg gagagcttcc ttcttgtggt catggcctat      360

gaccgctatg tggccatttg ctttcctttg cgttacacca ccatcatgag caccaagttc      420

tgtgcttcac tagtgctact tctgtggatg ctgacgatga cccatgccct gctgcatacc      480

ctactcattg ctagattgtc tttttgtgag aagaatgtga ttcttcactt tttctgtgac      540

atttctgctc ttctgaagtt gtcctgctca gacatttatg ttaatgagct gatgatatat      600

atcttgggtg gactcatcat tattatccca ttcctattaa ttgttatgtc ctatgttaga      660

attttcttct ccatttttgaa gtttccatct attcaggaca tctacaaggt attctcaacc      720

tgtggttccc atctgtctgt ggtgaccttg ttttatggga caattttttgg tatctactta      780

tgtccatcag gtaataattc tactgtgaag gagattgcca tggctatgat gtacacagtg      840

gtgactccca tgctgaatcc cttcatctac agcctgagga acagagacat gaaaagggcc      900

ctaataagag ttatctgcac taagaaaatc tctctgtaa                            939


<210>   6
<211>   945
<212>   DNA
<213>   Rattus sp.

<400>   6
atgacagaag agaaccaaac tgtgatctcc cagttccttc tcctttttcct gcccatccccc     60

tcagagcacc agcacgtgtt ctacgccctg ttcctgtcca tgtacctcac cactgtcctg      120

gggaacctca tcatcatcat cctcattcac ctggactccc atctccacac acccatgtac      180
```

```
ttgtttctca gcaacttgtc cttctctgat ctctgctttt cctctgttac gatgcccaag    240

ttgttgcaga acatgcagag ccaagttcca tccatcccct ttgcaggctg cctgacacaa    300

ttatactttt acctgtattt tgcagacctt gagagcttcc tgcttgtggc catggcctat    360

gaccgctatg tggccatctg cttccccctt cattacatga gcatcatgag ccccaagctc    420

tgtgtgagtc tggtggtgct gtcctgggtg ctgaccacct ccatgccat gctgcacacc      480

ctgctcatgg ccagattgtc attctgtgcg acaatatga tcccccactt tttctgtgat      540

atatctcctt tattgaaact gtcctgctct gacacgcatg ttaatgagtt ggtgatattt    600

gtcatgggag ggcttgttat tgtcattcca tttgtgctca tcattgtatc ttatgcacga    660

gttgtcgcct ccattcttaa agtcccttct gtccgaggca tccacaagat cttctccacc    720

tgcggctccc atctgtctgt ggtgtcactg ttctatggga caatcattgg tctctactta    780

tgtccgtcag ctaataactc tactgtgaag gagactgtca tggccatgat gtacacagtg    840

gtgacccca tgctgaaccc cttcatctac agcctgagga acagagacat gaaagaggca     900

ctgataagag tcctttgtaa aaagaaaatt accttctgtc tatga                    945


<210>  7
<211>  933
<212>  DNA
<213>  Rattus sp.

<400>  7
atgaacaatc aaactttcat cacccaattc cttctcctgg gactgcccat ccctgaagaa    60

catcagcacc tgttctatgc cttgttcctg gtcatgtacc tcaccaccat cttgggaaac    120

ttgctaatca ttgtacttgt tcaactggac tcccagctcc acacacctat gtatttgttt    180

ctcagcaatt tgtctttctc tgatctatgt tttttcctctg tcacaatgcc caagctgctg   240

cagaacatga ggagccagga cacatccatt ccctatggag ctgcctggc acaaacatac     300

ttctttatgg ttttttggaga tatggagagt ttccttcttg tggccatggc ctatgaccgc    360

tatgtggcca tctgcttccc tctgcattac accagcatca tgagccccaa gctctgtact    420

tgtctagtgc tgttattgtg gatgctgacg acatcccatg ccatgatgca cacactgctt    480

gcagcaagat tgtcttttttg tgagaacaat gtggtcctca acttcttctg tgacctattt    540

gttctcctaa agctggcctg ctcagacact tatattaatg agttgatgat atttatcatg    600

agtacactcc tcattattat tccattcttc ctcattgtta tgtcctatgc aaggatcata    660

tcctctattc ttaaggttcc atctacccaa ggcatctgca aggtcttctc tacctgtggt    720
```

tcccatctgt ctgtagtatc actgttctat gggacaatta ttggtctcta cttatgtcca   780

gcaggtaata attccactgt aaaagagatg gtcatggcca tgatgtacac tgtggtgacc   840

cccatgctga atcccttcat ctacagccta aggaatagag atatgaagag ggccctaata   900

agagttatct gtagtatgaa aatcactctg taa   933

<210> 8
<211> 984
<212> DNA
<213> Rattus sp.

<400> 8
atggagcgaa ggaaccacag tgggagagtg agtgaatttg tgttgctggg tttcccagct   60

cctgccccac tgcgagtact actatttttc ctttctcttc tggactatgt gttggtgttg   120

actgaaaaca tgctcatcat tatagcaatt aggaaccacc caaccctcca caaacccatg   180

tatttttct tggctaatat gtcatttctg gagatttggt atgtcactgt tacgattcct   240

aagatgctcg ctggcttcat tggttccaag gagaaccatg gacagctgat ctcctttgag   300

gcatgcatga cacaactcta cttttcctg ggcttgggtt gcacagagtg tgtccttctt   360

gctgtgatgg cctatgaccg ctatgtggct atctgtcatc cactccacta ccccgtcatt   420

gtcagtagcc ggctatgtgt gcagatggca gctggatcct gggctggagg ttttggtatc   480

tccatggtta aagttttcct tatttctcgc ctgtcttact gtggccccaa caccatcaac   540

cacttttct gtgatgtgtc tccattgctc aacctgtcat gcactgacat gtccacagca   600

gagcttacag actttgtcct ggccatttt attctgctgg accgctctc tgtcactggg   660

gcatcctaca tggccatcac aggtgctgtg atgcgcatcc cctcagctgc tggccgccat   720

aaagcctttt caacctgtgc ctcccacctc actgttgtga tcatcttcta tgcagccagt   780

attttcatct atgccaggcc taaggcactc tcagcttttg acaccaacaa gctggtctct   840

gtactctacg ctgtcattgt accgttgttc aatcccatca tctactgctt gcgcaaccaa   900

gatgtcaaaa gagcgctacg tcgcacgctg cacctggccc aggaccagga ggccaatacc   960

aacaaaggca gcaaaattgg ttag   984

<210> 9
<211> 939
<212> DNA
<213> Rattus sp.

<400> 9
atgaacaaca aaactgtcat cacccatttc ctcctcctgg gattgcccat ccccccagag   60

```
caccagcaac tgttctttgc cctgttcctg atcatgtacc tcaccacctt tctgggaaac    120

ctgctaattg ttgtccttgt tcaactggac tctcatctcc acacacccat gtacttgttt    180

ctcagcaact tgtccttctc tgatctctgc ttttcctctg ttacaatgct gaaattgctg    240

caaaatatac agagccaagt accatctata tcctatgcag gatgcctgac acagatattc    300

ttcttttttgt tgtttggcta ccttgggaat ttccttcttg tagccatggc ctatgaccgc    360

tatgtggcca tctgcttccc tctgcattat accaacatca tgagccataa gctctgtact    420

tgtctcctgc tggtattttg dataatgaca tcatctcatg ccatgatgca caccctgctt    480

gcagcaagat tgtcttttttg tgagaacaat gtactcctca acttttttctg tgacctgttt    540

gttctcctaa agttggcctg ctcagacact tatgttaatg agttgatgat acatatcatg    600

ggcgtgatca tcattgttat tccattcgtg ctcattgtta tatcctatgc caagatcatc    660

tcctccattc ttaaggttcc atctactcaa agcattcaca aggtcttctc cacttgtggt    720

tctcatctct ctgtggtgtc tctgttctac gggacaatta ttggtctcta tttatgtcca    780

tcaggtgata atttttagtct aaagggggtct gccatggcta tgatgtacac agtggtaact    840

ccaatgctga acccgttcat ctacagccta agaaacagag acatgaagca ggccctaata    900

agagttacct gtagcaagaa aatctctctg ccatggtag                          939
```

<210>   10
<211>   945
<212>   DNA
<213>   Rattus sp.

<400>   10
```
atgactagaa gaaaccaaac tgccatctct cagttcttcc ttctgggcct gccattcccc     60

ccagagtacc aacacctgtt ctatgccctg ttcctggcca tgtacctcac cactctcctg    120

gggaacctca tcatcatcat cctcattcta ctggactccc atctccacac acccatgtac    180

ttgtttctca gcaatttatc ctttgccgac ctctgttttt cctctgtcac aatgcccaag    240

ttgttgcaga acatgcagag ccaagttcca tccatcccct atgcagggtg cctggcacag    300

atatacttct ttctgttttt tggagacctt ggaaacttcc tgcttgtggc catggcctat    360

gaccgctatg tggccatctg cttcccccctt cattacatga gcatcatgag ccccaagctc    420

tgtgtgagtc tggtggtgct gtcctgggtg ctgactacct tccatgccat gctgcacacc    480

ctgctcatgg ccagattgtc attctgtgag dacagtgtga tccctcacta tttctgtgat    540

atgtctactc tgctgaaagt ggcttgttct gacacccatg ataatgaatt agcaatattt    600
```

atcttagggg gccctatagt tgtactacct ttccttctca tcattgtttc ttatgcaaga   660

attgtttcct ccatcttcaa ggtcccttct tctcaaagca tccataaagc cttctccacc   720

tgtggctccc acctgtctgt ggtgtcactg ttctatggga cagtcattgg tctctactta   780

tgtccttcag ctaataactc cactgtgaag gagactgtca tgtctttgat gtacacaatg   840

gtgacaccca tgctgaaccc cttcatctac agcctaagaa acagagacat aaaagatgca   900

ttagaaaaaa taatgtgcaa aaagcaaatt ccctcctttc tatga   945

<210> 11
<211> 645
<212> DNA
<213> Rattus sp.

<220>
<221> misc_feature
<222> (440)..(441)
<223> n = unknown

<400> 11
atctgttttg tgtctaccac tgtcccaaag cagctggtga acatccagac acagagcaga   60

gtcatcacct atgcagactg catcacccag atgtgctttt ttatactctt tgtagtgttg   120

gacagcttac tcctgactgt gatggcctat gaccggtttg tggccatctg tcaccccctg   180

cactacacag tcattatgag ctcctggctc tgtggactgc tggttctggt gtcctggatc   240

gtgagcatcc tatattctct gttacaaagc ataatggcat tgcagctgtc cttctgtaca   300

gaactgaaaa tccctcaatt tttctgtgaa cttaatcagg tcatccacct tgcctgttcc   360

gacactttta ttaatgacat gatgatgaat tttacaagtg tgctgctggg tggggatgc   420

ctcgctggaa tatttttactn ntactttaag atactttgtt gcatatgttc gatctcatca   480

gctcagggga tgaataaagc actttccacc tgtgcatctc acctctcagt tgtctcctta   540

ttttattgta caggcgtagg tgtgtacctt agttctgctg caacccataa ctcactctca   600

aatgctgcag cctcggtgat gtacactgtg gtcacctcca tgctg   645

<210> 12
<211> 215
<212> PRT
<213> Rattus sp.

<220>
<221> MISC_FEATURE
<222> (147)..(147)

<223>   x = unknown

<400>   12

Ile Cys Phe Val Ser Thr Thr Val Pro Lys Gln Leu Val Asn Ile Gln
1   5   10   15

Thr Gln Ser Arg Val Ile Thr Tyr Ala Asp Cys Ile Thr Gln Met Cys
            20   25   30

Phe Phe Ile Leu Phe Val Val Leu Asp Ser Leu Leu Leu Thr Val Met
        35   40   45

Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His Tyr Thr Val
        50   55   60

Ile Met Ser Ser Trp Leu Cys Gly Leu Leu Val Leu Val Ser Trp Ile
65   70   75   80

Val Ser Ile Leu Tyr Ser Leu Leu Gln Ser Ile Met Ala Leu Gln Leu
                85   90   95

Ser Phe Cys Thr Glu Leu Lys Ile Pro Gln Phe Phe Cys Glu Leu Asn
            100   105   110

Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Ile Asn Asp Met Met
            115   120   125

Met Asn Phe Thr Ser Val Leu Leu Gly Gly Gly Cys Leu Ala Gly Ile
    130   135   140

Phe Tyr Xaa Tyr Phe Lys Ile Leu Cys Cys Ile Cys Ser Ile Ser Ser
145   150   155   160

Ala Gln Gly Met Asn Lys Ala Leu Ser Thr Cys Ala Ser His Leu Ser
            165   170   175

Val Val Ser Leu Phe Tyr Cys Thr Gly Val Gly Val Tyr Leu Ser Ser
            180   185   190

Ala Ala Thr His Asn Ser Leu Ser Asn Ala Ala Ala Ser Val Met Tyr
        195   200   205

Thr Val Val Thr Ser Met Leu
    210   215

<210> 13
<211> 640
<212> DNA
<213> Rattus sp.

<220>
<221> misc_feature
<222> (182)..(182)
<223> n = unknown

<220>
<221> misc_feature
<222> (205)..(428)
<223> n = unknown

<220>
<221> misc_feature
<222> (494)..(495)
<223> n = unknown

<400> 13
catctgcttt acttctgcta gcatcccaaa gatgctagtg aatatacaga cgaagaacaa   60

ggtgatcacc tatgaaggct gcatctccca agtatacttt tcatactctt tggagttttg   120

gacaactttc ttctcgactg tgatggccta tgaccgatat gtggccatct gtcacccatc   180

tnactacaca ggtcatcatg aaccnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   240

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   300

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   360

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   420

nnnnnnnntt tattcttact ctaagatagt ttcctccata cgagaaatct catcatcaca   480

gggaaagtac aagnnattct ccacctgtgc atcccacctc tcagttgttt cattattcta   540

ttctacactt ttgggtgtgt accttagttc ttcttttacc caaaactcac actcaactgc   600

acgggcatct gttatgtaca gtgtggtcac ccccatgttg   640

<210> 14
<211> 213
<212> PRT
<213> Rattus sp.

<220>

<221> MISC_FEATURE
<222> (61)..(61)
<223> x = uknown

<220>
<221> MISC_FEATURE
<222> (68)..(143)
<223> x = unknown

<220>
<221> MISC_FEATURE
<222> (165)..(165)
<223> x = unknown

<400> 14

```
Ile Cys Phe Thr Ser Ala Ser Ile Pro Lys Met Leu Val Asn Ile Gln
1               5                   10                  15


Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile Ser Gln Val Tyr
            20                  25                  30


Phe Ser Tyr Ser Leu Glu Phe Trp Thr Thr Phe Phe Ser Thr Val Met
            35                  40                  45


Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Ser Xaa Tyr Thr Gly
            50                  55                  60


His His Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65                  70                  75                  80


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            85                  90                  95


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            100                 105                 110


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            115                 120                 125


Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Ser Tyr Ser
            130                 135                 140


Lys Ile Val Ser Ser Ile Arg Glu Ile Ala Glu Ile Ser Ser Ser Gln
145                 150                 155                 160
```

```
Gly Lys Tyr Lys Xaa Phe Ser Thr Cys Ala Ser His Leu Ser Val Val
                165             170             175

Ser Leu Phe Tyr Ser Thr Leu Leu Gly Val Tyr Leu Ser Ser Ser Phe
                180             185             190

Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser Val Met Tyr Ser Val
            195             200             205

Val Thr Pro Met Leu
    210


<210>   15
<211>   636
<212>   DNA
<213>   Rattus sp.

<400>   15
acctccacca ccatcccaaa gatgctggta aatatacaca cccagagcaa tactatcacc        60

tatgaagact gtatttccca gatgtttgta ctcttggttt ttggagaact ggacaacttt       120

ctcctggctg tgatggccta tgatcgatat gtggctatct gtcacccact gtattacaca       180

gtcattgtga accaccgact ctgtatcctg ctgcttctgc tgtcctgggt tgtcagcatt       240

ttacatgcct tcttacagag cttaattgta ctacagttga ccttctgtgg agatgtgaaa       300

atccctcact tcttctgtga gctcaatcag ctgtcccaac tcacatgttc agacaacttt       360

ccaagtcacc tcacaatgca tcttgtacct gttatatttg cagctatttc cctcagtggt       420

atcctttact cttatttcaa gatagtgtct tccatacgtt ctatgtcctc agttcaaggg       480

aagtacaagg cattttctac atgtgcctct cacctttcca ttgtctcctt attttatagt       540

acaggcctcg gggtgtacgt cagttctgct gtgatccgaa gctcacactc ctctgcaagt       600

gcttcggtca tgtatactgt ggtcaccccc atgttg                                 636


<210>   16
<211>   212
<212>   PRT
<213>   Rattus sp.

<400>   16

Thr Ser Thr Thr Ile Pro Lys Met Leu Val Asn Ile His Thr Gln Ser
1               5               10              15
```

```
Asn Thr Ile Thr Tyr Glu Asp Cys Ile Ser Gln Met Phe Val Leu Leu
        20              25              30

Val Phe Gly Glu Leu Asp Asn Phe Leu Leu Ala Val Met Ala Tyr Asp
        35              40              45

Arg Tyr Val Ala Ile Cys His Pro Leu Tyr Tyr Thr Val Ile Val Asn
    50              55              60

His Arg Leu Cys Ile Leu Leu Leu Leu Ser Trp Val Val Ser Ile
65              70              75              80

Leu His Ala Phe Leu Gln Ser Leu Ile Val Leu Gln Leu Thr Phe Cys
            85              90              95

Gly Asp Val Lys Ile Pro His Phe Phe Cys Glu Leu Asn Gln Leu Ser
            100             105             110

Gln Leu Thr Cys Ser Asp Asn Phe Pro Ser His Leu Thr Met His Leu
        115             120             125

Val Pro Val Ile Phe Ala Ala Ile Ser Leu Ser Gly Ile Leu Tyr Ser
    130             135             140

Tyr Phe Lys Ile Val Ser Ser Ile Arg Ser Met Ser Ser Val Gln Gly
145             150             155             160

Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser His Leu Ser Ile Val Ser
            165             170             175

Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr Val Ser Ser Ala Val Ile
            180             185             190

Arg Ser Ser His Ser Ser Ala Ser Ala Ser Val Met Tyr Thr Val Val
        195             200             205

Thr Pro Met Leu
    210


<210>  17
<211>  646
<212>  DNA
<213>  Rattus sp.
```

<400> 17

```
cataggctat tcatcttctg tcacacccaa tatgcttgtc aacttcctta taaagcaaaa      60

taccatctca taccttggat gttctataca gtttggctca gctgctttgt ttggaggtct     120

tgaatgcttc cttctggctg ccatggcgta tgatcgtttt gtagcaatct gcaacccact     180

gctttattca acgaaaatgt ccacacaagt ctgtgtccag ttggttgtgg gatcttatat     240

agggggattt cttaatgcct cctcttttac cctttccttt ttttccttgt ccttctgtgg     300

accaaataga atcaatcact tttactgtga ttttgctccg ttagtagaac tttcttgctc     360

tgatgtcagt gttcctgatg ctgttacctc attttctgct gcctcagtta ctatgctcac     420

agtgtttatc atagccatct cctataccta tatcctcatc accatcctga agatgcgttc     480

cactgagggt cgacagaaag cattctctac ctgcacttcc cacctcactg cagtcactct     540

gtgctatgga accatcacat tcatctatgt gatgcccaag tccagctact ccacagacca     600

gaacaaggtg gtgtctgtgt tttatatggt ggtgatcccc atgttg                    646
```

<210> 18
<211> 215
<212> PRT
<213> Rattus sp.

<400> 18

```
Ile Gly Tyr Ser Ser Ser Val Thr Pro Asn Met Leu Val Asn Phe Leu
1               5                   10                  15


Ile Lys Gln Asn Thr Ile Ser Tyr Leu Gly Cys Ser Ile Gln Phe Gly
                20                  25                  30


Ser Ala Ala Leu Pro Gly Gly Leu Glu Cys Phe Leu Leu Ala Ala Met
            35                  40                  45


Ala Tyr Asp Arg Phe Val Ala Ile Cys Asn Pro Leu Leu Tyr Ser Thr
        50                  55                  60


Lys Met Ser Thr Gln Val Cys Val Gln Leu Val Val Gly Ser Tyr Ile
65                  70                  75                  80


Gly Gly Phe Leu Asn Ala Ser Ser Phe Thr Leu Ser Phe Phe Ser Leu
                85                  90                  95


Ser Phe Cys Gly Pro Asn Arg Ile Asn His Phe Tyr Cys Asp Phe Ala
```

100   105   110

Pro Leu Val Glu Leu Ser Cys Ser Asp Val Ser Val Pro Asp Ala Val
        115   120   125

Thr Ser Phe Ser Ala Ala Ser Val Thr Met Leu Thr Val Phe Ile Ile
        130   135   140

Ala Ile Ser Tyr Thr Tyr Ile Leu Ile Thr Ile Leu Lys Met Arg Ser
145   150   155   160

Thr Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Thr Ser His Leu Thr
     .   165   170   175

Ala Val Thr Leu Cys Tyr Gly Thr Ile Thr Phe Ile Tyr Val Met Pro
                180   185   190

Lys Ser Ser Tyr Ser Thr Asp Gln Asn Lys Val Val Ser Val Phe Tyr
        195   200   205

Met Val Val Ile Pro Met Leu
    210   215

<210> 19
<211> 481
<212> DNA
<213> Rattus sp.

<400> 19
catctgcaag cccctgcact acaccaccat catgaataac cgagtgtgca cagttctagt   60

cctctcctgt tggtttgctg gcctgttgat catcctccca cctcttggtc atggcctcca   120

gctggagttc tgtgactcca atgtgattga tcattttggc tgtgatgcct ctccaattct   180

gcagataacc tgctcagaca cggtatttat agagaaaatt gtcttggctt ttgccatact   240

gacactcatc attactctgg tatgtgttgt tctctcctac acatacatca tcaagaccat   300

tttaaagttt ccttctgctc aacaaagaaa aaaggccttt tctacatgtt cttcccacat   360

gattgtggtt tccatcacct atgggagctg tattttcatc tacatcaaac cttcagcgaa   420

ggaaggggta gccatcaata aggttgtatc tgtgctcaca acatcagtcg cccctttgct   480

c   481

<210> 20

<211> 160
<212> PRT
<213> Rattus sp.

<400> 20

Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Asn Asn Arg Val Cys
1   5   10   15

Thr Val Leu Val Leu Ser Cys Trp Phe Ala Gly Leu Leu Ile Ile Leu
            20   25   30

Pro Pro Leu Gly His Gly Leu Gln Leu Glu Phe Cys Asp Ser Asn Val
        35   40   45

Ile Asp His Phe Gly Cys Asp Ala Ser Pro Ile Leu Gln Ile Thr Cys
        50   55   60

Ser Asp Thr Val Phe Ile Glu Lys Ile Val Leu Ala Phe Ala Ile Leu
65   70   75   80

Thr Leu Ile Ile Thr Leu Val Cys Val Val Leu Ser Tyr Thr Tyr Ile
                85   90   95

Ile Lys Thr Ile Leu Lys Phe Pro Ser Ala Gln Gln Arg Lys Lys Ala
                100   105   110

Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr Tyr Gly
            115   120   125

Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Gly Val Ala
        130   135   140

Ile Asn Lys Val Val Ser Val Leu Thr Thr Ser Val Ala Pro Leu Leu
145   150   155   160

<210> 21
<211> 481
<212> DNA
<213> Rattus sp.

<220>
<221> misc_feature
<222> (270)..(274)
<223> n = unknown

<400> 21
catctgccac ccgctccact actctcttct catgagtcct gacaactgtg ctgctctggt   60

aacagtctcc tgggtgacag gggtgggcac gggcttcctg ccttccctcc tgatttctaa   120

gttggacttc tgtgggccca accgcatcaa ccatttcttc tgtgacctcc ctccattaat   180

ccagctgtcc tgctccagcg tctttgtgac agaaatggcc atctttgtcc tgtccatcgc   240

tgtgctctgc atctgtttcc tcctaacccn nnnntcctac attttcatag tgtcctccat   300

tctgagaatc ccttccacta ccggcaggat gaagacattt tctacatgtg gctcccacct   360

ggccgtggtc accatctact atgggaccat gatctccatg tatgtcggcc caaatgcgca   420

tctgtccccg gagctcaaca aggtcatttc tgtcttctac actgtgatca ccccactact   480

g   481

<210> 22
<211> 160
<212> PRT
<213> Rattus sp.

<220>
<221> MISC_FEATURE
<222> (90)..(91)
<223> x = unknown

<400> 22

Ile Cys His Pro Leu His Tyr Ser Leu Leu Met Ser Pro Asp Asn Cys
1   5   10   15

Ala Ala Leu Val Thr Val Ser Trp Val Thr Gly Val Gly Thr Gly Phe
            20   25   30

Leu Pro Ser Leu Leu Ile Ser Lys Leu Asp Phe Cys Gly Pro Asn Arg
        35   40   45

Ile Asn His Phe Phe Cys Asp Leu Pro Pro Leu Ile Gln Leu Ser Cys
    50   55   60

Ser Ser Val Phe Val Thr Glu Met Ala Ile Phe Val Leu Ser Ile Ala
65   70   75   80

Val Leu Cys Ile Cys Phe Leu Leu Thr Xaa Xaa Ser Tyr Ile Phe Ile
                85   90   95

```
Val Ser Ser Ile Leu Arg Ile Pro Ser Thr Thr Gly Arg Met Lys Thr
        100                 105                 110

Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Thr Ile Tyr Tyr Gly
        115                 120                 125

Thr Met Ile Ser Met Tyr Val Gly Pro Asn Ala His Leu Ser Pro Glu
    130                 135                 140

Leu Asn Lys Val Ile Ser Val Phe Tyr Thr Val Ile Thr Pro Leu Leu
145                 150                 155                 160


<210>   23
<211>   646
<212>   DNA
<213>   Rattus sp.

<220>
<221>   misc_feature
<222>   (1)..(1)
<223>   n = unknown


<220>
<221>   misc_feature
<222>   (236)..(402)
<223>   n = unknown


<400>   23
ngtctgcttc tcctccacca ctgtccccaa ggtactggct aaccacatac tcagtagtca      60

ggccatttcc ttctctgggt gtctaactca gctgtatttt ctctgtgtgt ctgtgaatat     120

ggacaatttc ctgctggctg tgatggccta tgacagattt gtggccatat gccacccttt     180

gtactacaca acaaagatga cccaccagct ctgtgtcttg ctggtgtctg gatcannnnn     240

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     300

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn     360

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nntgtgatca tggtcacccc     420

atttgtctgc atcctcatct cttacatcta catcaccaat gcagtcctca gagtctcatc     480

ctttagggga ggatggaaag ccttctccac ctgtggctca cacctggctg tggtctgcct     540

cttctatggc accatcattg ctgtgtattt caatcctgta tcttcccatt catctgagaa     600

ggacactgca gcaactgtgc tatacacagt ggtgactccc atgttg                   646
```

<210> 24
<211> 215
<212> PRT
<213> Rattus sp.

<220>
<221> MISC_FEATURE
<222> (79)..(134)
<223> x = unknown

<400> 24

Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala Asn His Ile
1   5   10   15

Leu Ser Ser Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr Gln Leu Tyr
                20   25   30

Phe Leu Cys Val Ser Val Asn Met Asp Asn Phe Leu Leu Ala Val Met
        35   40   45

Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Tyr Tyr Thr Thr
    50   55   60

Lys Met Thr His Gln Leu Cys Val Leu Leu Val Ser Gly Ser Xaa Xaa
65   70   75   80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                85   90   95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                100   105   110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
                115   120   125

Xaa Xaa Xaa Xaa Xaa Xaa Val Ile Met Val Thr Pro Phe Val Cys Ile
        130   135   140

Leu Ile Ser Tyr Ile Tyr Ile Thr Asn Ala Val Leu Arg Val Ser Ser
145   150   155   160

Phe Arg Gly Gly Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala
                165   170   175

```
Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Ala Val Tyr Phe Asn Pro
          180                 185                 190


Val Ser Ser His Ser Ser Glu Lys Asp Thr Ala Ala Thr Val Leu Tyr
          195                 200                 205


Thr Val Val Thr Pro Met Leu
    210                 215
```

```
<210>   25
<211>   646
<212>   DNA
<213>   Rattus sp.

<220>
<221>   misc_feature
<222>   (236)..(402)
<223>   n = unknown


<400>   25
tgtctgcttc tcctccacca ctgtccccaa ggtactggct aaccacatac tcagtagtca     60

ggccatttcc ttctctgggt gtctaactca gctgtatttt ctctgtgtgt ctgtgaatat    120

ggacaatttc ctgctggctg tgatggccta tgacagattt gtggccatat gccacccttt    180

gtactacaca acaccgatga cccaccagct ctgtgtcttg ctggtgtctg gatcannnnn    240

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    300

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn    360

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nntgtgatca tggtcacccc    420

atttgtctgc atcctcatct cttacatcta catcaccaat gcagtcctca gagtctcatc    480

ctttagggga ggatggaaag ccttctccac ctgtggctca cacctggctg tggtctgcct    540

cttctatggc accatcattg ctgtgtattt caatcctgta tcttcccatt catctgagaa    600

ggacactgca gcaactgtgc tatacacagt ggtgactccc atgttg                   646
```

```
<210>   26
<211>   215
<212>   PRT
<213>   Rattus sp.

<220>
<221>   MISC_FEATURE
<222>   (79)..(134)
<223>   x = unknown
```

<400> 26

Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala Asn His Ile
1   5   10   15

Leu Ser Ser Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr Gln Leu Tyr
                20   25   30

Phe Leu Cys Val Ser Val Asn Met Asp Asn Phe Leu Leu Ala Val Met
        35   40   45

Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Tyr Tyr Thr Thr
    50   55   60

Pro Met Thr His Gln Leu Cys Val Leu Leu Val Ser Gly Ser Xaa Xaa
65   70   75   80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            85   90   95

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            100   105   110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
        115   120   125

Xaa Xaa Xaa Xaa Xaa Xaa Val Ile Met Val Thr Pro Phe Val Cys Ile
    130   135   140

Leu Ile Ser Tyr Ile Tyr Ile Thr Asn Ala Val Leu Arg Val Ser Ser
145   150   155   160

Phe Arg Gly Gly Trp Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ala
            165   170   175

Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Ala Val Tyr Phe Asn Pro
        180   185   190

Val Ser Ser His Ser Ser Glu Lys Asp Thr Ala Ala Thr Val Leu Tyr
        195   200   205

Thr Val Val Thr Pro Met Leu
    210   215

<210> 27
<211> 481
<212> DNA
<213> Rattus sp.

<220>
<221> misc_feature
<222> (183)..(185)
<223> n = unknown

<400> 27
tatctgcaac cctctgcgct acccagtgct catgagcggc cgggtgtgcc tgctcatggt   60

cgtggcctcc tggttgggag gatccctcaa cgcctccatt cagacttctc tgacccttca   120

gttcccctac tgtggatcac ggaagatctc ccacttcttc tgtgaggtgc cctcgctgct   180

gannntggcc tgtgcagaca ctgaagccta tgagcaggta ctatttgtga caggcgtggt   240

ggtcctcctg gtgcccatta cattcattac tgcctcttat gccctcatcc tggctgctgt   300

gctccgaatg cactctgcgg aggggagtca gaaggcccta gccacatgct cctctcacct   360

gacagtcgtc aatctcttct atgggcccct tgtctacacc tacatgttac ctgcttccta   420

tcactcacca ggccaagacg acatagtatc cgtcttttac accgttctca cacccatgct   480

t   481

<210> 28
<211> 160
<212> PRT
<213> Rattus sp.

<220>
<221> MISC_FEATURE
<222> (61)..(62)
<223> x = unknown

<400> 28

Ile Cys Asn Pro Leu Arg Tyr Pro Val Leu Met Ser Gly Arg Val Cys
1   5   10   15

Leu Leu Met Val Val Ala Ser Trp Leu Gly Gly Ser Leu Asn Ala Ser
            20   25   30

Ile Gln Thr Ser Leu Thr Leu Gln Phe Pro Tyr Cys Gly Ser Arg Lys
        35   40   45

```
Ile Ser His Phe Phe Cys Glu Val Pro Ser Leu Leu Xaa Xaa Ala Cys
    50                  55                  60

Ala Asp Thr Glu Ala Tyr Glu Gln Val Leu Phe Val Thr Gly Val Val
65                  70                  75                  80

Val Leu Leu Val Pro Ile Thr Phe Ile Thr Ala Ser Tyr Ala Leu Ile
                85                  90                  95

Leu Ala Ala Val Leu Arg Met His Ser Ala Glu Gly Ser Gln Lys Ala
                100                 105                 110

Leu Ala Thr Cys Ser Ser His Leu Thr Val Val Asn Leu Phe Tyr Gly
            115                 120                 125

Pro Leu Val Tyr Thr Tyr Met Leu Pro Ala Cys Tyr His Ser Pro Gly
    130                 135                 140

Gln Asp Asp Ile Val Ser Val Phe Tyr Thr Val Leu Thr Pro Met Leu
145                 150                 155                 160
```

<210> 29
<211> 481
<212> DNA
<213> Rattus sp.

<400> 29
```
catctgtagg cctcttcact atcctaccct catgacccag acactgtgtg ccaagattgc      60

cactggttgc tggttgggag gcttggctgg gccagtggta gaaatttcct tggtgtctcg     120

tctcctttttt tgtggcccca atcacattca acacatcttt tgtgatttcc cacctgtgct     180

gagcttggct tgtactgata catcagtgaa tgtcctggta gattttatta taaacctctg     240

caagatcctg gccaccttcc tgctgatcct gagctcctac ttgcagataa tccgcacagt     300

gctcaagatt ccttcagctg caggcaagaa gaaagcattc tcgacttgtg cctcccatct     360

cactgtggtt ctcatcttct atgggagcat cctttttcatg tatgtgcggc tgaagaagac     420

ttactccctt gactacgaca gagccttggc agtagtctac tccgtggtta cccctttcct     480

g                                                                       481
```

<210> 30
<211> 160
<212> PRT

<213> Rattus sp.

<400> 30

Ile Cys Arg Pro Leu His Tyr Pro Thr Leu Met Thr Gln Thr Leu Cys
1   5   10   15

Ala Lys Ile Ala Thr Gly Cys Trp Leu Gly Gly Leu Ala Gly Pro Val
            20   25   30

Val Glu Ile Ser Leu Val Ser Arg Leu Leu Phe Cys Gly Pro Asn His
        35   40   45

Ile Gln His Ile Phe Cys Asp Phe Pro Pro Val Leu Ser Leu Ala Cys
    50   55   60

Thr Asp Thr Ser Val Asn Val Leu Val Asp Phe Ile Ile Asn Leu Cys
65   70   75   80

Lys Ile Leu Ala Thr Phe Leu Leu Ile Leu Ser Ser Tyr Leu Gln Ile
            85   90   95

Ile Arg Thr Val Leu Lys Ile Pro Ser Ala Ala Gly Lys Lys Lys Ala
            100   105   110

Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Leu Ile Phe Tyr Gly
        115   120   125

Ser Ile Leu Phe Met Tyr Val Arg Leu Lys Lys Thr Tyr Ser Leu Asp
    130   135   140

Tyr Asp Arg Ala Leu Ala Val Val Tyr Ser Val Val Thr Pro Phe Leu
145   150   155.   160

<210> 31
<211> 481
<212> DNA
<213> Rattus sp.

<220>
<221> misc_feature
<222> (178)..(179)
<223> n = unknown

<400> 31
aatctgcaac ccactgcttt attccaccaa aatgtccaca caagtctgta tccagttggt   60

```
tgcaggatct tatatagggg gttttcttaa tacttgcctc atcatgtttt actttttctc      120

ttttctcttc tgtgggccaa atatagttga tcattttttc tgtgattttg ctcctttnnt      180

ggaactttcg tgctctgatg tgagtgtctc tgtagttgtt atgtcatttt ctgctggctc      240

agttactatg atcacagtgt ttatcatagc catctcctat tcttacatcc tcatcaccat      300

cctgaagatg tcctcaactg agggccgtca caaggctttc tccacatgta cctcccacct      360

cactgcagtc actctctact atggcaccat taccttcatt tatgtgatgc ccaagtccac      420

atactctaca gaccagaaca aggtggtgtc tgtgttttac atggtggtga tcccaatgtt      480

g                                                                      481


<210>  32
<211>  160
<212>  PRT
<213>  Rattus sp.

<220>
<221>  MISC_FEATURE
<222>  (59)..(60)
<223>  x = unknown


<400>  32

Ile Cys Asn Pro Leu Leu Tyr Ser Thr Lys Met Ser Thr Gln Val Cys
1               5                  10                  15


Ile Gln Leu Val Ala Gly Ser Tyr Ile Gly Gly Phe Leu Asn Thr Cys
            20                  25                  30


Leu Ile Met Phe Tyr Phe Phe Ser Phe Leu Phe Cys Gly Pro Asn Ile
            35                  40                  45


Val Asp His Phe Phe Cys Asp Phe Ala Pro Xaa Xaa Glu Leu Ser Cys
        50                  55                  60


Ser Asp Val Ser Val Ser Val Val Val Met Ser Phe Ser Ala Gly Ser
65                  70                  75                  80


Val Thr Met Ile Thr Val Phe Ile Ile Ala Ile Ser Tyr Ser Tyr Ile
                85                  90                  95


Leu Ile Thr Ile Leu Lys Met Ser Ser Thr Glu Gly Arg His Lys Ala
                100                 105                 110
```

Phe Ser Thr Cys Thr Ser His Leu Thr Ala Val Thr Leu Tyr Tyr Gly
        115   120   125

Thr Ile Thr Phe Ile Tyr Val Met Pro Lys Ser Thr Tyr Ser Thr Asp
        130   135   140

Gln Asn Lys Val Val Ser Val Phe Tyr Met Val Val Ile Pro Met Leu
145   150   155   160

<210> 33
<211> 479
<212> DNA
<213> Rattus sp.

<400> 33
tatctgccac cctctgaagt acacagttat catgaatcac tatttttgtg tgatgctgct   60

gctcttctct gtgttcgtta gcattgcaca tgcgttgttc cacattttaa tggtgttgat   120

actgactttc agcacaaaaa ctgaaatccc tcactttttc tgtgagctgg ctcatatcat   180

caaacttacc tgttccgata atttttatcaa ctatctgctg atatacacag agtctgtctt   240

attttttggt gttcatattg tagggatcat tttgtcttat atttacactg tatcctcagt   300

tttaagaatg tcattattgg gaggaatgta taaagccttt tcaacatgtg gatctcattt   360

gtcggttgtc tctgttttat ggcacaggtt ttggggtaca cataagctct ccacttactg   420

actctccaag gaagactgta gtggcttcag tgatgtacac tgtggttact cagatgctg   479

<210> 34
<211> 139
<212> PRT
<213> Rattus sp.

<400> 34

Ile Cys His Pro Leu Lys Tyr Thr Val Ile Met Asn His Tyr Phe Cys
1   5   10   15

Val Met Leu Leu Leu Phe Ser Val Phe Val Ser Ile Ala His Ala Leu
                20   25   30

Phe His Ile Leu Met Val Leu Ile Leu Thr Phe Ser Thr Lys Thr Glu
        35   40   45

Ile Pro His Phe Phe Cys Glu Leu Ala His Ile Ile Lys Leu Thr Cys

Ser Asp Asn Phe Ile Asn Tyr Leu Leu Ile Tyr Thr Glu Ser Val Leu
65   70   75   80

Phe Phe Gly Val His Ile Val Gly Ile Ile Leu Ser Tyr Ile Tyr Thr
                85   90   95

Val Ser Ser Val Leu Arg Met Ser Leu Leu Gly Gly Met Tyr Lys Ala
            100   105   110

Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Val Leu Trp His
        115   120   125

Arg Phe Trp Gly Thr His Lys Leu Ser Thr Tyr
    130   135

<210>   35
<211>   481
<212>   DNA
<213>   Rattus sp.

<220>
<221>   misc_feature
<222>   (212)..(253)
<223>   n = unknown

<400>   35
aatctgctac ccactgaggt accttctcat catgagctgg gtggtgtgca cagcactgtc   60

cgtggcaatc tgggtcatag gcttttgtgc ctccgttata cctctctgct tcacgatcct   120

cccactctgt ggtccttacg tcgttgatta tcttttctgc gagctgccca tccttctgca   180

cctgttctgc acagatacat ctctgctgga gnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   240

nnnnnnnnnn nnnccttcc tcctgattgt tctctcctac cttcgcatcc tggtggctgt   300

gataagaata gactcagctg agggcagaaa aaaggccttt tcaacttgtg cttcacactt   360

ggctgtggtg accatctact atggaacagg gctgatcagg tacttgaggc ccaagtccct   420

ttattccgct gagggagaca gactgatctc tgtgttctat gcagtcattg ccctgcact   480

g   481

<210>   36
<211>   160
<212>   PRT

<213> Rattus sp.

<220>
<221> MISC_FEATURE
<222> (71)..(84)
<223> x = unknown

<400> 36

Ile Cys Tyr Pro Leu Arg Tyr Leu Leu Ile Met Ser Trp Val Val Cys
1   5   10   15

Thr Ala Leu Ser Val Ala Ile Trp Val Ile Gly Phe Cys Ala Ser Val
                20   25   30

Ile Pro Leu Cys Phe Thr Ile Leu Pro Leu Cys Gly Pro Tyr Val Val
        35   40   45

Asp Tyr Leu Phe Cys Glu Leu Pro Ile Leu Leu His Leu Phe Cys Thr
        50   55   60

Asp Thr Ser Leu Leu Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65   70   75   80

Xaa Xaa Xaa Xaa Pro Phe Leu Leu Ile Val Leu Ser Tyr Leu Arg Ile
                85   90   95

Leu Val Ala Val Ile Arg Ile Asp Ser Ala Glu Gly Arg Lys Lys Ala
                100   105   110

Phe Ser Thr Cys Ala Ser His Leu Ala Val Val Thr Ile Tyr Tyr Gly
        115   120   125

Thr Gly Leu Ile Arg Tyr Leu Arg Pro Lys Ser Leu Tyr Ser Ala Glu
        130   135   140

Gly Asp Arg Leu Ile Ser Val Phe Tyr Ala Val Ile Gly Pro Ala Leu
.145   150   155   160

<210> 37
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer directed to members of the 7 transmembrane domain protein

superfamily

```
<220>
<221>  misc_feature
<222>  (9)..(9)
<223>  n = any


<220>
<221>  misc_feature
<222>  (12)..(12)
<223>  n = any


<220>
<221>  misc_feature
<222>  (15)..(15)
<223>  n = any


<220>
<221>  misc_feature
<222>  (21)..(21)
<223>  n = any


<220>
<221>  misc_feature
<222>  (24)..(24)
<223>  n = any


<220>
<221>  misc_feature
<222>  (27)..(27)
<223>  n = any


<220>
<221>  misc_feature
<222>  (30)..(30)
<223>  n = any


<220>
<221>  misc_feature
<222>  (33)..(33)
<223>  n = any


<400>  37
aattggatnc tngtnaatct ngcngtngcn gcnga                                    35


<210>  38
<211>  32
<212>  DNA
```

```
<213>   Artificial Sequence

<220>
<223>   Primer directed to members of the 7 transmembrane domain protein
        superfamily

<220>
<221>   misc_feature
<222>   (12)..(12)
<223>   n = any


<220>
<221>   misc_feature
<222>   (15)..(15)
<223>   n = any


<220>
<221>   misc_feature
<222>   (21)..(21)
<223>   n = any


<220>
<221>   misc_feature
<222>   (24)..(24)
<223>   n = any


<220>
<221>   misc_feature
<222>   (27)..(27)
<223>   n = any


<220>
<221>   misc_feature
<222>   (30)..(30)
<223>   n = any


<400>   38
aattattttc tngtnaatct ngcnttngcn ga                                      32


<210>   39
<211>   32
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Primer directed to members of the 7 transmembrane domain protein
        superfamily

<220>
<221>   misc_feature
```

```
<222>  (6)..(6)
<223>  n = any


<220>
<221>  misc_feature
<222>  (12)..(12)
<223>  n = any


<220>
<221>  misc_feature
<222>  (15)..(15)
<223>  n = any


<220>
<221>  misc_feature
<222>  (18)..(18)
<223>  n = any


<220>
<221>  misc_feature
<222>  (21)..(21)
<223>  n = any


<220>
<221>  misc_feature
<222>  (24)..(24)
<223>  n = any


<220>
<221>  misc_feature
<222>  (27)..(27)
<223>  n = any


<220>
<221>  misc_feature
<222>  (30)..(30)
<223>  n = any


<400>  39
aatttnttta tnatntcnct ngcntgngcn ga                                  32


<210>  40
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer directed to members of the 7 transmembrane domain protein
```

```
         superfamily

<220>
<221>   misc_feature
<222>   (3)..(3)
<223>   n = any


<220>
<221>   misc_feature
<222>   (6)..(6)
<223>   n = any


<220>
<221>   misc_feature
<222>   (9)..(9)
<223>   n = any


<220>
<221>   misc_feature
<222>   (21)..(21)
<223>   n = any


<220>
<221>   misc_feature
<222>   (30)..(30)
<223>   n = any


<400>   40
cgnttnctna tgtgtaacct ntgctttgcn ga                                          32


<210>   41
<211>   32
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Primer directed to members of the 7 transmembrane domain protein
        superfamily

<220>
<221>   misc_feature
<222>   (3)..(3)
<223>   n = any


<220>
<221>   misc_feature
<222>   (6)..(6)
<223>   n = any
```

```
<220>
<221>  misc_feature
<222>  (12)..(12)
<223>  n = any


<220>
<221>  misc_feature
<222>  (15)..(15)
<223>  n = any


<220>
<221>  misc_feature
<222>  (21)..(21)
<223>  n = any


<220>
<221>  misc_feature
<222>  (24)..(24)
<223>  n = any


<220>
<221>  misc_feature
<222>  (27)..(27)
<223>  n = any


<220>
<221>  misc_feature
<222>  (30)..(30)
<223>  n = any


<400>  41
acngtntata tnacncatct nacnatngcn ga                                    32


<210>  42
<211>  33
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer directed to members of the 7 transmembrane domain protein
       superfamily

<220>
<221>  misc_feature
<222>  (4)..(4)
<223>  n = any


<220>
<221>  misc_feature
```

<222> (13)..(13)
<223> n = any

<220>
<221> misc_feature
<222> (16)..(16)
<223> n = any

<220>
<221> misc_feature
<222> (22)..(22)
<223> n = any

<220>
<221> misc_feature
<222> (25)..(25)
<223> n = any

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = any

<400> 42
ctgncggttc atnaanacat anatnatngg gtt   33

<210> 43
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer directed to members of the 7 transmembrane domain protein
       superfamily

<220>
<221> misc_feature
<222> (8)..(8)
<223> n = any

<220>
<221> misc_feature
<222> (20)..(20)
<223> n = any

<220>
<221> misc_feature
<222> (23)..(23)
<223> n = any

```
<220>
<221>  misc_feature
<222>  (26)..(26)
<223>  n = any


<400>  43
gatcgttnag acaacaatan atnatngggt t                                31


<210>  44
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer directed to members of the 7 transmembrane domain protein
       superfamily

<220>
<221>  misc_feature
<222>  (3)..(3)
<223>  n = any


<220>
<221>  misc_feature
<222>  (12)..(12)
<223>  n = any


<220>
<221>  misc_feature
<222>  (15)..(15)
<223>  n = any


<220>
<221>  misc_feature
<222>  (21)..(21)
<223>  n = any


<220>
<221>  misc_feature
<222>  (24)..(24)
<223>  n = any


<220>
<221>  misc_feature
<222>  (27)..(27)
<223>  n = any
```

<400> 44
tcnatgttaa angtngtata natnatnggg tt   32

<210> 45
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer directed to members of the 7 transmembrane domain protein
      superfamily

<220>
<221> misc_feature
<222> (6)..(6)
<223> n = any

<220>
<221> misc_feature
<222> (12)..(12)
<223> n = any

<220>
<221> misc_feature
<222> (15)..(15)
<223> n = any

<220>
<221> misc_feature
<222> (21)..(21)
<223> n = any

<220>
<221> misc_feature
<222> (27)..(27)
<223> n = any

<400> 45
gccttngtaa anatngcata naggaanggg tt   32

<210> 46
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer directed to members of the 7 transmembrane domain protein
      superfamily

<220>

```
<221>  misc_feature
<222>  (6)..(6)
<223>  n = any


<220>
<221>  misc_feature
<222>  (12)..(12)
<223>  n = any


<220>
<221>  misc_feature
<222>  (15)..(15)
<223>  n = any


<220>
<221>  misc_feature
<222>  (21)..(21)
<223>  n = any


<220>
<221>  misc_feature
<222>  (26)..(26)
<223>  n = any


<220>
<221>  misc_feature
<222>  (27)..(27)
<223>  n = any


<400>  46
aaatcngggc tncgncaata natcannggg tt                                          32


<210>  47
<211>  32
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer directed to members of the 7 transmembrane domain protein
       superfamily

<220>
<221>  misc_feature
<222>  (3)..(3)
<223>  n = any


<220>
<221>  misc_feature
<222>  (6)..(6)
```

```
<223>  n = any


<220>
<221>  misc_feature
<222>  (9)..(9)
<223>  n = any


<220>
<221>  misc_feature
<222>  (21)..(21)
<223>  n = any


<220>
<221>  misc_feature
<222>  (27)..(27)
<223>  n = any


<400>  47
ganganccna caaaaaaata nataaanggg tt                                    32


<210>  48
<211>  23
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer directed to members of the 7 transmembrane domain protein
       superfamily

<220>
<221>  misc_feature
<222>  (6)..(6)
<223>  n = any


<220>
<221>  misc_feature
<222>  (15)..(15)
<223>  n = any


<220>
<221>  misc_feature
<222>  (21)..(21)
<223>  n = any


<400>  48
atggcntatg atcgntatgt ngc                                              23


<210>  49
```

```
<211>  29
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer directed to members of the 7 transmembrane domain protein
       superfamily

<220>
<221>  misc_feature
<222>  (3)..(3)
<223>  n = any


<220>
<221>  misc_feature
<222>  (6)..(6)
<223>  n = any


<220>
<221>  misc_feature
<222>  (9)..(9)
<223>  n = any


<220>
<221>  misc_feature
<222>  (12)..(12)
<223>  n = any


<220>
<221>  misc_feature
<222>  (15)..(15)
<223>  n = any


<220>
<221>  misc_feature
<222>  (18)..(18)
<223>  n = any


<220>
<221>  misc_feature
<222>  (24)..(24)
<223>  n = any


<220>
<221>  misc_feature
<222>  (27)..(27)
<223>  n = any


<400>  49
```

<210> 50
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence motif found at the N-terminus of the cytoplasmic loop in
      certain odorant receptor protein clones

<400> 50

Lys Ile Val Ser Ser Ile
1   5

<210> 51
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence motif found at the N-terminus of the cytoplasmic loop in
      certain odorant receptor protein clones

<400> 51

Arg Ile Val Ser Ser Ile
1   5

<210> 52
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence motif found at the N-terminus of the cytoplasmic loop in
      certain odorant receptor protein clones

<400> 52

His Ile Thr Cys Ala Val
1   5

<210> 53
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence motif found at the N-terminus of the cytoplasmic loop in
      certain odorant receptor protein clones

<400> 53

His Ile Thr Trp Ala Val
1   5

<210> 54
<211> 19
<212> PRT
<213> Rattus sp.

<400> 54

Leu Ser Lys Glu Asp Cys Ser Gly Phe Ser Asp Val His Cys Gly Tyr
1   5   10   15

Ser Asp Ala

<210> 55
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the loop between the first transmembrane
      domain and the second transmembrane domain, and the second transm
      embrane domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> x = any

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> x = any

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> x = any

<400> 55

Leu Xaa Xaa Pro Met Tyr Xaa Phe Leu
1   5

<210> 56
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the loop between the first transmembrane
domain and the second transmembrane domain, and the second transm
embrane domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> H or Q

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> K or M or T

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> F or L

<400> 56

Leu Xaa Xaa Pro Met Tyr Xaa Phe Leu
1   5

<210> 57
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the third transmembrane domain, and the l
oop between the third transmembrane domain and the fourth transme
mbrane domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> x = any

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> x = any

<220>
<221> MISC_FEATURE
<222> (7)..(7)

<223> x = any

<400> 57

Met Xaa Tyr Asp Arg Xaa Xaa Ala Ile Cys
1   5   10

<210> 58
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the third transmembrane domain, and the l
      oop between the third transmembrane domain and the fourth transme
      mbrane domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> A or S

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> F or Y

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> L or V

<400> 58

Met Xaa Tyr Asp Ala Xaa Xaa Ala Ile Cys
1   5   10

<210> 59
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the third transmembrane domain, and the l
      oop between the third transmembrane domain and the fourth transme
      mbrane domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> x = any

```
<220>
<221>  MISC_FEATURE
<222>  (4)..(4)
<223>  x = any


<400>  59

Asp Arg Xaa Xaa Ala Ile Cys
1               5


<210>  60
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Amino acid sequence for the third transmembrane domain, and the l
       oop between the third transmembrane domain and the fourth transme
       mbrane domain of an odorant receptor protein

<220>
<221>  MISC_FEATURE
<222>  (3)..(3)
<223>  F or Y


<220>
<221>  MISC_FEATURE
<222>  (4)..(4)
<223>  L or V


<400>  60

Asp Arg Xaa Xaa Ala Ile Cys
1               5


<210>  61
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Amino acid sequence for the loop between the fifth transmembrane
       domain and the sixth transmembrane domain, and the sixth transmem
       brane domain of an odorant receptor protein

<220>
<221>  MISC_FEATURE
<222>  (1)..(1)
<223>  K or R
```

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> x = any

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> x = any

<400> 61

Xaa Xaa Phe Ser Thr Cys Xaa Ser His
1   5

<210> 62
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the loop between the fifth transmembrane
      domain and the sixth transmembrane domain, and the sixth transmem
      brane domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> K or R

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> A or I or S or V

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> A or G or S

<400> 62

Xaa Xaa Phe Ser Thr Cys Xaa Ser His
1   5

<210> 63
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the loop between the fifth transmembrane
       domain and the sixth transmembrane domain, and the sixth transmem
       brane domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> x = any

<400> 63

Phe Ser Thr Cys Xaa Ser His
1   5

<210> 64
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the loop between the fifth transmembrane
       domain and the sixth transmembrane domain, and the sixth transmem
       brane domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> A or G or S

<400> 64

Phe Ser Thr Cys Xaa Ser His
1   5

<210> 65
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the seventh transmembrane domain and the
       C-terminal domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> x = any

<220>
<221> MISC_FEATURE

```
<222>   (3)..(3)
<223>   x = any


<220>
<221>   MISC_FEATURE
<222>   (6)..(6)
<223>   x = any


<220>
<221>   MISC_FEATURE
<222>   (9)..(9)
<223>   x = any


<400>   65

Pro Xaa Xaa Asn Pro Xaa Ile Tyr Xaa Leu Arg Asn
1               5                   10


<210>   66
<211>   12
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Amino acid sequence for the seventh transmembrane domain and the
        C-terminal domain of an odorant receptor protein

<220>
<221>   MISC_FEATURE
<222>   (2)..(2)
<223>   M or L or V


<220>
<221>   MISC_FEATURE
<222>   (3)..(3)
<223>   F or L or V


<220>
<221>   MISC_FEATURE
<222>   (6)..(6)
<223>   F or I


<220>
<221>   MISC_FEATURE
<222>   (9)..(9)
<223>   C or S or T


<400>   66
```

```
Pro Xaa Xaa Asn Pro Xaa Ile Tyr Xaa Leu Arg Asn
1               5               10
```

<210> 67
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the seventh transmembrane domain and the
       C-terminal domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> x = any

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> x = any

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> x = any

<400> 67

```
Pro Xaa Xaa Asn Pro Xaa Ile Tyr
1               5
```

<210> 68
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence for the seventh transmembrane domain and the
       C-terminal domain of an odorant receptor protein

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> M or L or V

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> F or L or V

```
<220>
<221>  MISC_FEATURE
<222>  (6)..(6)
<223>  F or !


<400>  68

Pro Xaa Xaa Asn Pro Xaa Ile Tyr
1               5


<210>  69
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Amino acid sequence for the seventh transmembrane domain and the
       C-terminal domain of an odorant receptor protein

<220>
<221>  MISC_FEATURE
<222>  (3)..(3)
<223>  x = any


<220>
<221>  MISC_FEATURE
<222>  (6)..(6)
<223>  x = any


<400>  69

Asn Pro Xaa Ile Tyr Xaa Leu Arg Asn
1               5


<210>  70
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Amino acid sequence for the seventh transmembrane domain and the
       C-terminal domain of an odorant receptor protein

<220>
<221>  MISC_FEATURE
<222>  (3)..(3)
<223>  F or I


<220>
<221>  MISC_FEATURE
```

<222> (6)..(6)
<223> C or S or T

<400> 70

Asn Pro Xaa Ile Tyr Xaa Leu Arg Asn
1   5

<210> 71
<211> 333
<212> PRT
<213> Rattus sp.

<400> 71

Met Asp Ser Ser Asn Arg Thr Arg Val Ser Glu Phe Leu Leu Leu Gly
1   5   10   15

Phe Val Glu Asn Lys Asp Leu Gln Pro Leu Ile Tyr Gly Leu Phe Leu
            20   25   30

Ser Met Tyr Leu Val Thr Val Ile Gly Asn Ile Ser Ile Ile Val Ala
        35   40   45

Ile Ile Ser Asp Pro Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ser
    50   55   60

Asn Leu Ser Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys
65   70   75   80

Met Leu Val Asn Ile Gln Thr Gln Asn Asn Val Ile Thr Tyr Ala Gly
                85   90   95

Cys Ile Thr Gln Ile Tyr Phe Phe Leu Leu Phe Cys Glu Leu Asp Asn
            100   105   110

Phe Leu Leu Thr Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His
        115   120   125

Pro Met His Tyr Thr Val Ile Met Asn Tyr Lys Leu Cys Gly Phe Leu
    130   135   140

Val Leu Val Ser Trp Ile Val Ser Val Leu His Ala Leu Phe Gln Ser
145   150   155   160

Leu Met Met Leu Ala Leu Pro Phe Cys Thr His Leu Glu Ile Pro His
            165   170   175

Tyr Phe Cys Glu Pro Asn Gln Val Ile Gln Leu Thr Cys Ser Asp Ala
            180   185   190

Phe Leu Asn Asp Leu Val Ile Tyr Phe Thr Leu Val Leu Leu Ala Thr
            195   200   205

Val Pro Leu Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Val Ser Ser
        210   215   220

Ile Cys Ala Ile Ser Ser Val His Gly Lys Tyr Lys Ala Phe Ser Thr
225   230   235   240

Cys Ala Ser His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu
                245   250   255

Gly Val Tyr Leu Ser Ser Ala Ala Asn Asn Ser Ser Gln Ala Ser Ala
            260   265   270

Thr Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Val Asn Pro Phe
            275   280   285

Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Ser Val Leu Lys Lys Thr
        290   295   300

Leu Cys Glu Glu Val Ile Arg Ser Pro Pro Ser Leu Leu His Phe Phe
305   310   315   320

Leu Val Leu Cys His Leu Pro Cys Phe Ile Phe Cys Tyr
                325   330

<210> 72
<211> 313
<212> PRT
<213> Rattus sp.

<400> 72

Met Ser Ser Thr Asn Gln Ser Ser Val Thr Glu Phe Leu Leu Leu Gly
1   5   10   15

Leu Ser Arg Gln Pro Gln Gln Gln Leu Leu Phe Leu Leu Phe Leu
            20   25   30

```
Ile Met Tyr Leu Ala Thr Val Leu Gly Asn Leu Leu Ile Ile Leu Ala
        35                  40                  45


Ile Gly Thr Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu Ser
        50                  55                  60


Asn Leu Ser Phe Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys
65                  70                  75                  80


Val Leu Ala Asn His Ile Leu Gly Ser Gln Ala Ile Ser Phe Ser Gly
                85                  90                  95


Cys Leu Thr Gln Leu Tyr Phe Leu Ala Val Phe Gly Asn Met Asp Asn
            100                 105                 110


Phe Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Val Ala Ile Cys His
        115                 120                 125


Pro Leu His Tyr Thr Thr Lys Met Thr Arg Gln Leu Cys Val Leu Leu
        130                 135                 140


Val Val Gly Ser Trp Val Val Ala Asn Met Asn Cys Leu Leu His Ile
145                 150                 155                 160


Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Ser Asn Met Ile Pro His
                165                 170                 175


Phe Phe Cys Asp Gly Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
            180                 185                 190


His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val
        195                 200                 205


Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala
        210                 215                 220


Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys Ser Phe Ser Thr
225                 230                 235                 240


Cys Gly Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile
                245                 250                 255
```

Ala Val Tyr Phe Asn Pro Ser Ser Ser His Leu Ala Gly Arg Asp Met
        260   265   270

Ala Ala Ala Val Met Tyr Ala Val Val Thr Pro Met Leu Asn Pro Phe
        275   280   285

Ile Tyr Ser Leu Arg Asn Ser Asp Met Lys Ala Ala Leu Arg Lys Val
        290   295   300

Leu Ala Met Arg Phe Pro Ser Lys Gln
305   310

<210>   73
<211>   311
<212>   PRT
<213>   Rattus sp.

<400>   73

Met Ala Trp Ser Thr Gly Gln Asn Leu Ser Thr Pro Gly Pro Phe Ile
1   5   10   15

Leu Leu Gly Phe Pro Gly Pro Arg Ser Met Arg Ile Gly Leu Phe Leu
        20   25   30

Leu Phe Leu Val Met Tyr Leu Leu Thr Val Val Gly Asn Leu Ala Ile
        35   40   45

Ile Ser Leu Val Gly Ala His Arg Cys Leu Gln Thr Pro Met Tyr Phe
        50   55   60

Phe Leu Cys Asn Leu Ser Phe Leu Glu Ile Trp Phe Thr Thr Ala Cys
65   70   75   80

Val Pro Lys Thr Leu Ala Thr Phe Ala Pro Arg Gly Gly Val Ile Ser
                85   90   95

Leu Ala Gly Cys Ala Thr Gln Met Tyr Phe Val Phe Ser Leu Gly Cys
            100   105   110

Thr Glu Tyr Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Leu Ala
        115   120   125

Ile Cys Leu Pro Leu Arg Tyr Gly Gly Ile Met Thr Pro Gly Leu Ala

Met Arg Leu Ala Leu Gly Ser Trp Leu Cys Gly Phe Ser Ala Ile Thr
145   150   155   160

Val Pro Ala Thr Leu Ile Ala Arg Leu Ser Phe Cys Gly Ser Arg Val
                165   170   175

Ile Asn His Phe Phe Cys Asp Ile Ser Pro Trp Ile Val Leu Ser Cys
            180   185   190

Thr Asp Thr Gln Val Val Glu Leu Val Ser Phe Gly Ile Ala Phe Cys
            195   200   205

Val Ile Leu Gly Ser Cys Gly Ile Thr Leu Val Ser Tyr Ala Tyr Ile
    210   215   220

Ile Thr Thr Ile Ile Lys Ile Pro Ser Ala Arg Gly Arg His Arg Ala
225   230   235   240

Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp Tyr Gly
            245   250   255

Ser Thr Ile Phe Leu His Val Arg Thr Ser Val Glu Ser Ser Leu Asp
            260   265   270

Leu Thr Lys Ala Ile Thr Val Leu Asn Thr Ile Val Thr Pro Val Leu
            275   280   285

Asn Pro Phe Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Glu Ala Leu
    290   295   300

Arg Arg Thr Val Lys Gly Lys
305   310

<210> 74
<211> 317
<212> PRT
<213> Rattus sp.

<400> 74

Met Glu Ser Gly Asn Ser Thr Arg Arg Phe Ser Ser Phe Phe Leu Leu
1   5   10   15

```
Gly Phe Thr Glu Asn Pro Gln Leu His Phe Leu Ile Phe Ala Leu Phe
        20              25              30

Leu Ser Met Tyr Leu Val Thr Val Leu Gly Asn Leu Leu Ile Ile Met
        35              40              45

Ala Ile Ile Thr Gln Ser His Leu His Thr Pro Met Tyr Phe Phe Leu
    50              55              60

Ala Asn Leu Ser Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro
65              70              75              80

Lys Met Leu Val Asn Ile Tyr Thr Gln Ser Lys Ser Ile Thr Tyr Glu
            85              90              95

Asp Cys Ile Ser Gln Met Cys Val Phe Leu Val Phe Ala Glu Leu Gly
            100             105             110

Asn Phe Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Asn Cys
        115             120             125

His Pro Leu Cys Tyr Thr Val Ile Val Asn His Arg Leu Cys Ile Leu
    130             135             140

Leu Leu Leu Leu Ser Trp Val Ile Ser Ile Phe His Ala Phe Ile Gln
145             150             155             160

Ser Leu Ile Val Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro
            165             170             175

His Phe Phe Cys Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Ser Asp
        180             185             190

Asn Phe Pro Ser His Leu Ile Met Asn Leu Val Pro Val Met Leu Ala
        195             200             205

Ala Ile Ser Phe Ser Gly Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser
    210             215             220

Ser Ile His Ser Ile Ser Thr Val Gln Gly Lys Tyr Lys Ala Phe Ser
225             230             235             240
```

Thr Cys Ala Ser His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly
                245   250   255

Leu Gly Val Tyr Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala
            260   265   270

Ala Ser Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro
        275   280   285

Phe Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Arg Ala Leu Glu Arg
    290   295   300

Leu Leu Glu Gly Asn Cys Lys Val His His Trp Thr Gly
305   310   315

<210> 75
<211> 310
<212> PRT
<213> Rattus sp.

<400> 75

Met Asn Asn Gln Thr Phe Ile Thr Gln Phe Leu Leu Leu Gly Leu Pro
1   5   10   15

Ile Pro Glu Glu His Gln His Leu Phe Tyr Ala Leu Phe Leu Val Met
            20   25   30

Tyr Leu Thr Thr Ile Leu Gly Asn Leu Leu Ile Ile Val Leu Val Gln
        35   40   45

Leu Asp Ser Gln Leu His Thr Pro Met Tyr Leu Phe Leu Ser Asn Leu
    50   55   60

Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu
65   70   75   80

Gln Asn Met Arg Ser Gln Asp Thr Ser Ile Pro Tyr Gly Gly Cys Leu
            85   90   95

Ala Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu
        100   105   110

Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
        115   120   125

His Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Thr Cys Leu Val Leu
    130   135   140

Leu Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu
145   150   155   160

Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Val Leu Asn Phe Phe
                165   170   175

Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Ile
            180   185   190

Asn Glu Leu Met Ile Phe Ile Met Ser Thr Leu Leu Ile Ile Ile Pro
        195   200   205

Phe Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu
    210   215   220

Lys Val Pro Ser Thr Gln Gly Ile Cys Leu Val Phe Ser Thr Cys Gly
225   230   235   240

Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu
                245   250   255

Tyr Leu Cys Pro Ala Gly Asn Asn Ser Thr Val Lys Glu Met Val Met
            260   265   270

Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
        275   280   285

Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val Ile Cys
    290   295   300

Ser Met Lys Ile Thr Leu
305   310

<210>   76
<211>   327
<212>   PRT
<213>   Rattus sp.

<400>   76

```
Met Glu Arg Arg Asn His Ser Gly Arg Val Ser Glu Phe Val Leu Leu
1               5               10              15

Gly Phe Pro Ala Pro Ala Pro Leu Arg Val Leu Leu Phe Phe Leu Ser
            20              25              30

Leu Leu Asp Tyr Val Leu Val Leu Thr Glu Asn Met Leu Ile Ile Ile
        35              40              45

Ala Ile Arg Asn His Pro Thr Leu His Lys Pro Met Tyr Phe Phe Leu
    50              55              60

Ala Asn Met Ser Phe Leu Glu Ile Trp Tyr Val Thr Val Thr Ile Pro
65              70              75              80

Lys Met Leu Ala Gly Phe Ile Gly Ser Lys Glu Asn His Gly Gln Leu
            85              90              95

Ile Ser Phe Glu Ala Cys Met Thr Gln Leu Tyr Phe Phe Leu Gly Leu
            100             105             110

Gly Cys Thr Glu Cys Val Leu Leu Ala Val Met Ala Tyr Asp Arg Tyr
        115             120             125

Val Ala Ile Cys His Pro Leu His Tyr Pro Val Ile Val Ser Ser Arg
    130             135             140

Leu Cys Val Gln Met Ala Ala Gly Ser Trp Ala Gly Gly Phe Gly Ile
145             150             155             160

Ser Met Val Lys Val Phe Leu Ile Ser Arg Leu Ser Tyr Cys Gly Pro
            165             170             175

Asn Thr Ile Asn His Phe Phe Cys Asp Val Ser Pro Leu Leu Asn Leu
            180             185             190

Ser Cys Thr Asp Met Ser Thr Ala Glu Leu Thr Asp Phe Val Leu Ala
        195             200             205

Ile Phe Ile Leu Leu Gly Pro Leu Ser Val Thr Gly Ala Ser Tyr Met
    210             215             220

Ala Ile Thr Gly Ala Val Met Arg Ile Pro Ser Ala Ala Gly Arg His
```

Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe
            245   250   255

Tyr Ala Ala Ser Ile Phe Ile Tyr Ala Arg Pro Lys Ala Leu Ser Ala
            260   265   270

Phe Asp Thr Asn Lys Leu Val Ser Val Leu Tyr Ala Val Ile Val Pro
            275   280   285

Leu Phe Asn Pro Ile Ile Tyr Cys Leu Arg Asn Gln Asp Val Lys Arg
    290   295   300

Ala Leu Arg Arg Thr Leu His Leu Ala Gln Asp Gln Glu Ala Asn Thr
305   310   315   320

Asn Lys Gly Ser Lys Ile Gly
                325

<210> 77
<211> 312
<212> PRT
<213> Rattus sp.

<400> 77

Met Asn Asn Lys Thr Val Ile Thr His Phe Leu Leu Leu Gly Leu Pro
1   5   10   15

Ile Pro Pro Glu His Gln Gln Leu Phe Phe Ala Leu Phe Leu Ile Met
            20   25   30

Tyr Leu Thr Thr Phe Leu Gly Asn Leu Leu Ile Val Val Leu Val Gln
        35   40   45

Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Pro Leu Ser Asn Leu
    50   55   60

Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Leu Lys Leu Leu
65   70   75   80

Gln Asn Ile Gln Ser Gln Val Pro Ser Ile Ser Tyr Ala Gly Cys Leu
                85   90   95

Thr Gln Ile Phe Phe Phe Leu Leu Phe Gly Tyr Leu Gly Asn Phe Leu
            100   105   110

Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu
            115   120   125

His Tyr Thr Asn Ile Met Ser His Lys Leu Cys Thr Cys Leu Leu Leu
        130   135   140

Asn Phe Trp Ile Met Thr Ser Ser His Ala Met Met His Thr Leu Leu
145   150   155   160

Ala Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Leu Leu Asn Phe Phe
                165   170   175

Cys Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val
            180   185   190

Asn Glu Leu Met Ile His Ile Met Gly Val Ile Ile Ile Val Ile Pro
        195   200   205

Phe Val Leu Ile Val Ile Ser Tyr Ala Lys Ile Ile Ser Ser Ile Leu
    210   215   220

Lys Val Pro Ser Thr Gln Ser Ile His Lys Val Phe Ser Thr Cys Gly
225   230   235   240

Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu
            245   250   255

Tyr Leu Cys Pro Ser Gly Asp Asn Phe Ser Leu Lys Gly Ser Ala Met
            260   265   270

Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe Ile Tyr
            275   280   285

Ser Leu Arg Asn Arg Asp Met Lys Gln Ala Leu Ile Arg Val Thr Cys
    290   295   300

Ser Lys Lys Ile Ser Leu Pro Trp
305   310

<210> 78
<211> 314
<212> PRT
<213> Rattus sp.

<400> 78

Met Thr Arg Arg Asn Gln Thr Ala Ile Ser Gln Phe Phe Leu Leu Gly
1   5   10   15

Leu Pro Phe Pro Pro Glu Tyr Gln His Leu Phe Tyr Ala Leu Phe Leu
            20   25   30

Ala Met Tyr Leu Thr Thr Leu Leu Gly Asn Leu Ile Ile Ile Ile Leu
        35   40   45

Ile Leu Leu Asp Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
    50   55   60

Asn Leu Ser Phe Ala Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65   70   75   80

Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly
                85   90   95

Cys Leu Ala Gln Ile Tyr Phe Phe Leu Phe Phe Gly Asp Leu Gly Asn
            100   105   110

Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
        115   120   125

Pro Leu His Tyr Met Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu
        130   135   140

Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
145   150   155   160

Leu Leu Met Ala Arg Leu Ser Phe Cys Glu Asp Ser Val Ile Pro His
                165   170   175

Tyr Phe Cys Asp Met Ser Thr Leu Leu Lys Val Ala Cys Ser Asp Thr
            180   185   190

His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val Val
        195   200   205

```
Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser Ser
    210             215             220

Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys Ala Phe Ser Thr
225             230             235             240

Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile
            245             250             255

Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr
            260             265             270

Val Met Ser Leu Met Tyr Thr Met Val Thr Pro Met Leu Asn Pro Phe
        275             280             285

Ile Tyr Ser Leu Arg Asn Arg Asp Ile Lys Asp Ala Leu Glu Lys Ile
    290             295             300

Met Cys Lys Lys Gln Ile Pro Ser Phe Leu
305             310


<210>  79
<211>  312
<212>  PRT
<213>  Rattus sp.

<400>  79

Met Thr Gly Asn Asn Gln Thr Leu Ile Leu Glu Phe Leu Leu Leu Gly
1               5               10              15

Leu Pro Ile Pro Ser Glu Tyr His Leu Leu Phe Tyr Ala Leu Phe Leu
            20              25              30

Ala Met Tyr Leu Thr Ile Ile Leu Gly Asn Leu Leu Ile Ile Val Leu
        35              40              45

Val Arg Leu Asp Ser His Leu His Met Pro Met Tyr Leu Phe Leu Ser
    50              55              60

Asn Leu Ser Phe Ser Asp Leu Cys Pro Ser Ser Val Thr Met Pro Lys
65              70              75              80
```

```
Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Ser Tyr Thr Gly
            85                  90                  95


Cys Leu Thr Gln Leu Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser
            100                 105                 110


Phe Leu Leu Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
            115                 120                 125


Pro Leu Arg Tyr Thr Thr Ile Met Ser Thr Lys Phe Cys Ala Ser Leu
    130                 135                 140


Val Leu Leu Leu Trp Met Leu Thr Met Thr His Ala Leu Leu His Thr
145                 150                 155                 160


Leu Leu Ile Ala Arg Leu Ser Phe Cys Glu Lys Asn Val Ile Leu His
            165                 170                 175


Phe Phe Cys Asp Ile Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Ile
            180                 185                 190


Tyr Val Asn Glu Leu Met Ile Tyr Ile Leu Gly Gly Leu Ile Ile Ile
    195                 200                 205


Ile Pro Phe Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser
    210                 215                 220


Ile Leu Lys Phe Pro Ser Ile Gln Asp Ile Tyr Lys Val Phe Ser Thr
225                 230                 235                 240


Cys Gly Ser His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Phe
            245                 250                 255


Gly Ile Tyr Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Glu Ile
            260                 265                 270


Ala Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
    275                 280                 285


Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Arg Ala Leu Ile Arg Val
    290                 295                 300


Ile Cys Thr Lys Lys Ile Ser Leu
```

<210> 80
<211> 314
<212> PRT
<213> Rattus sp.

<400> 80

Met Thr Glu Glu Asn Gln Thr Val Ile Ser Gln Phe Leu Leu Leu Phe
1   5   10   15

Leu Pro Ile Pro Ser Glu His Gln His Val Phe Tyr Ala Leu Phe Leu
            20   25   30

Ser Met Tyr Leu Thr Thr Val Leu Gly Asn Leu Ile Ile Ile Ile Leu
            35   40   45

Ile His Leu Ala Ser His Leu His Thr Pro Met Tyr Leu Phe Leu Ser
        50   55   60

Asn Leu Ser Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys
65   70   75   80

Leu Leu Gln Asn Met Gln Ser Gln Val Pro Ser Ile Pro Phe Ala Gly
                85   90   95

Cys Leu Thr Gln Leu Tyr Phe Tyr Leu Tyr Phe Ala Asp Leu Glu Ser
            100   105   110

Phe Leu Leu Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe
            115   120   125

Pro Leu His Tyr Met Ser Ile Met Ser Pro Tyr Leu Cys Val Ser Leu
        130   135   140

Val Val Leu Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr
145   150   155   160

Leu Leu Met Ala Arg Leu Ser Phe Cys Ala Asp Asn Met Ile Pro His
                165   170   175

Phe Phe Cys Asp Ile Ser Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr
            180   185   190

His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile Val
        195   200   205

Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala Ser
        210   215   220

Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys Ile Phe Ser Thr
225   230   235   240

Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
                245   250   255

Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr
            260   265   270

Val Met Ala Met Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
        275   280   285

Ile Tyr Ser Leu Arg Asn Arg Asp Met Lys Glu Ala Leu Ile Arg Val
        290   295   300

Leu Cys Lys Lys Lys Ile Thr Phe Cys Leu
305   310

<210> 81
<211> 44
<212> PRT
<213> Rattus sp.

<400> 81

Arg Val Asn Glu Val Val Ile Phe Ile Val Val Ser Leu Phe Leu Val
1   5   10   15

Leu Pro Phe Ala Leu Ile Ile Met Ser Tyr Val Arg Ile Val Ser Ser
            20   25   30

Ile Leu Lys Val Pro Ser Ser Gln Gly Ile Tyr Lys
        35   40

<210> 82
<211> 44
<212> PRT
<213> Rattus sp.

<400> 82

Phe Leu Asn Asp Leu Val Ile Tyr Phe Thr Leu Val Leu Leu Ala Thr
1   5   10   15

Val Pro Leu Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Val Ser Ser
            20   25   30

Ile Cys Ala Ile Ser Ser Val His Gly Lys Tyr Lys
            35   40

<210> 83
<211> 44
<212> PRT
<213> Rattus sp.

<400> 83

His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Thr
1   5   10   15

Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Cys Ala Val
            20   25   30

Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys
            35   40

<210> 84
<211> 44
<212> PRT
<213> Rattus sp.

<400> 84

Gln Val Val Glu Leu Val Ser Phe Gly Ile Ala Phe Cys Val Ile His
1   5   10   15

Gly Ser Cys Gly Ile Thr Leu Val Ser Tyr Ala Tyr Ile Ile Thr Thr
            20   25   30

Ile Ile Lys Ile Pro Ser Ala Arg Gly Arg His Arg
            35   40

<210> 85
<211> 44
<212> PRT
<213> Rattus sp.

<400> 85

His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Ile Ile Leu Val
1   5   10   15

Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Val Arg Ile Val Ser Ser
            20   25   30

Ile Leu Lys Val Pro Ser Ala Arg Gly Ile Arg Lys
        35   40

<210> 86
<211> 44
<212> PRT
<213> Rattus sp.

<400> 86

Phe Pro Ser His Leu Thr Met His Leu Val Pro Val Ile Leu Ala Ala
1   5   10   15

Ile Ser Leu Ser Gly Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser
            20   25   30

Ile Arg Ser Met Ser Ser Val Gln Gly Lys Tyr Lys
        35   40

<210> 87
<211> 44
<212> PRT
<213> Rattus sp.

<400> 87

Phe Pro Ser His Leu Ile Met Asn Leu Val Pro Val Met Leu Ala Ala
1   5   10   15

Ile Ser Phe Ser Gly Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser
            20   25   30

Ile His Ser Ile Ser Thr Val Gln Gly Lys Tyr Lys
        35   40

<210> 88
<211> 44
<212> PRT
<213> Rattus sp.

<400> 88

Phe Pro Ser His Leu Ile Met Asn Leu Val Pro Val Met Leu Ala Ala
1   5   10   15

Ile Ser Phe Ser Gly Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser
            20   25   30

Ile Arg Ser Val Ser Ser Val Lys Gly Lys Tyr Lys
        35   40

<210> 89
<211> 44
<212> PRT
<213> Rattus sp.

<400> 89

Phe Leu Asn Asp Val Ile Met Tyr Phe Ala Leu Val Leu Leu Ala Val
1   5   10   15

Val Pro Leu Leu Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser
            20   25   30

Ile Arg Ala Ile Ser Thr Val Gln Gly Lys Tyr Lys
        35   40

<210> 90
<211> 44
<212> PRT
<213> Rattus sp.

<400> 90

His Glu Ile Glu Met Ile Ile Leu Val Leu Ala Ala Phe Asn Leu Ile
1   5   10   15

Ser Ser Leu Leu Val Val Leu Val Ser Tyr Leu Phe Ile Leu Ile Ala
            20   25   30

Ile Leu Arg Met Asn Ser Ala Glu Gly Arg Arg Lys
        35   40

<210> 91
<211> 44
<212> PRT
<213> Rattus sp.

<400> 91

Tyr Ile Asn Glu Leu Met Ile Phe Ile Met Ser Thr Leu Leu Ile Ile
1   5   10   15

Ile Pro Phe Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ser Ser
            20   25   30

Ile Leu Lys Val Pro Ser Thr Gln Gly Ile Cys Lys
        35   40

<210> 92
<211> 44
<212> PRT
<213> Rattus sp.

<400> 92

Ser Thr Ala Glu Leu Thr Asp Phe Val Leu Ala Ile Phe Ile Leu Leu
1   5   10   15

Gly Pro Leu Ser Val Thr Gly Ala Ser Tyr Met Ala Ile Thr Gly Ala
            20   25   30

Val Met Arg Ile Pro Ser Ala Ala Gly Arg His Lys
        35   40

<210> 93
<211> 44
<212> PRT
<213> Rattus sp.

<400> 93

Tyr Val Asn Glu Leu Met Ile His Ile Met Gly Val Ile Ile Ile Val
1   5   10   15

Ile Pro Phe Val Leu Ile Val Ile Ser Tyr Ala Lys Ile Ile Ser Ser
            20   25   30

Ile Leu Lys Val Pro Ser Thr Gln Ser Ile His Lys
        35   40

<210> 94
<211> 44
<212> PRT
<213> Rattus sp.

<400> 94

His Asp Asn Glu Leu Ala Ile Phe Ile Leu Gly Gly Pro Ile Val Val
1   5   10   15

Leu Pro Phe Leu Leu Ile Ile Val Ser Tyr Ala Arg Ile Val Ser Ser
            20   25   30

Ile Phe Lys Val Pro Ser Ser Gln Ser Ile His Lys
            35   40

<210>   95
<211>   44
<212>   PRT
<213>   Rattus sp.

<400>   95

His Leu Asn Glu Leu Met Ile Leu Thr Glu Gly Ala Val Val Met Val
1   5   10   15

Thr Pro Phe Val Cys Ile Leu Ile Ser Tyr Ile His Ile Thr Trp Ala
            20   25   30

Val Leu Arg Val Ser Ser Pro Arg Gly Gly Trp Lys
            35   40

<210>   96
<211>   44
<212>   PRT
<213>   Rattus sp.

<400>   96

Phe Pro Ser His Leu Ile Met Asn Leu Val Pro Val Met Leu Gly Ala
1   5   10   15

Ile Ser Leu Ser Gly Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser
            20   25   30

Val Arg Ser Ile Ser Ser Val Gln Gly Lys His Lys
            35   40

<210>   97
<211>   44
<212>   PRT
<213>   Rattus sp.

<400> 97

Tyr Val Asn Glu Leu Met Ile Tyr Ile Leu Gly Gly Leu Ile Ile Ile
1   5   10   15

Ile Pro Phe Leu Leu Ile Val Met Ser Tyr Val Arg Ile Phe Phe Ser
            20   25   30

Ile Leu Lys Phe Pro Ser Ile Glx Asp Ile Tyr Lys
            35   40

<210>   98
<211>   44
<212>   PRT
<213>   Rattus sp.

<400>   98

His Val Asn Glu Leu Val Ile Phe Val Met Gly Gly Leu Val Ile Val
1   5   10   15

Ile Pro Phe Val Leu Ile Ile Val Ser Tyr Ala Arg Val Val Ala Ser
            20   25   30

Ile Leu Lys Val Pro Ser Val Arg Gly Ile His Lys
            35   40